

CRF Errors Corrected by the STIC System Branch

7/17 #6 OPE
7/31/02

Serial Number: 10/084,553

CRF Processing Date: _____
 Edited by: _____
 Verified by: DC (STIC staff)

- ENTERED
- ☐ Changed a file from non-ASCII to ASCII
 - ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
 - ☐ Edited a format error in the Current Application Data section, specifically: _____
 - ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____
 - ☐ Added the mandatory heading and subheadings for "Current Application Data".
 - ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
 - ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____
 - ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: _____
 - ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: _____
 - ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
 - ☐ Inserted colons after headings/subheadings. Headings edited included: _____
 - ☐ Deleted extra, invalid, headings used by an applicant, specifically: _____
 - ☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as _____
 - ☒ Inserted mandatory headings, specifically: L2207 in Seq. 2
 - ☐ Corrected an obvious error in the response, specifically: _____
 - ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
 - ☐ Corrected an error in the Number of Sequences field, specifically: _____
 - ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
 - ☐ Deleted **ending** stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____
 - ☐ Other: _____

*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.



OIPE

RAW SEQUENCE LISTING

DATE: 07/31/2002

PATENT APPLICATION: US/10/084,553

TIME: 12:41:33

Input Set : A:\PTO.DC.txt

Output Set: N:\CRF3\07312002\J084553.raw

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3 <110> APPLICANT: Tobin, Elaine
4      Wang, Zhi-Yong
5      Sun, Lin
6      The Regents of the University of California
8 <120> TITLE OF INVENTION: Phytochrome Regulated Transcription Factor for Control
9      of Higher Plant Development
11 <130> FILE REFERENCE: 023070-124200US
13 <140> CURRENT APPLICATION NUMBER: US 10/084,553
C--> 14 <141> CURRENT FILING DATE: 2002-07-09
16 <150> PRIOR APPLICATION NUMBER: US 08/843,572
17 <151> PRIOR FILING DATE: 1997-04-18
19 <160> NUMBER OF SEQ ID NOS: 27
21 <170> SOFTWARE: PatentIn Ver. 2.1
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 4344
25 <212> TYPE: DNA
26 <213> ORGANISM: Arabidopsis thaliana
28 <220> FEATURE:
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30      genomic clone
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58 <222> LOCATION: (2190)..(2384)
60 <220> FEATURE:
61 <221> NAME/KEY: intron

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89 tgtttgttat ctgtttcagg gaggtttgt ttgagaaggt caagagcaca tacaaagaca 180
91 tattaggagg cagctgaatc aaaggaggaa gaagaagaag aagagccttt ttgaggccat 240
93 tcatgaattg gaatgaagga tatcaaaaga atctaacaca aaggccacgt cttccttca 300
95 atctttcctt cttgtaaacta aataattttc atcctttctc tctctctgtc tctgggtctt 360
97 tttagctcaa agtatcatcc atttatgtca aagtgttgta aattcctcaa gactatatat 420
99 gagatgtttt gtttcatttt ccaaaatttc aaactttgtc cccatttagt cttctaccct 480
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103 aaaagaacaa aaccttatgg gtctaaaaaa aataagccca atataaaaact atggcccaaa 600
105 taagtttagg tccattagag tgtgagaata gcgctgttag tgaaccgcac gagaatgcgc 660
107 gtctgattgt tgggtgaagta gtcgtctaga ttcccgggtc cactgatgtt tctagtgtat 720
109 cagacacgtg tcgacaaact ggtgggagag attaacgatc ttaagtaggt cccactagat 780
111 caagatatta taacgaattg acctttttaa cctttcaggt agtcccggaa ctctgtgacct 840
113 agaatacaaa gaaggttggtg aacaagttga tgtaagatg gacaagaatg taacttgaac 900
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125 tacttaagat tgatttattg tcatgggtctt tcttattggt tgatgaataa cttgacttga 1260
127 ttgttttttg ttttgtggat tagtggaatt ttgtaaagag aagatctgaa gttgtgtaga 1320
129 ggagcttagt g atg gag aca aat tcg tct gga gaa gat ctg gtt att aag 1370
130 Met Glu Thr Asn Ser Ser Gly Glu Asp Leu Val Ile Lys
131 1 5 10
133 gtaaattaac taaatttttag ggggaagatg attgttttag gtgtcaaaga ttgagaattt 1430
135 taatgaaact tgatatag act cgg aag cca tat acg ata aca aag caa cgt 1481
136 Thr Arg Lys Pro Tyr Thr Ile Thr Lys Gln Arg
137 15 20
139 gaa agg tgg act gag gaa gaa cat aat aga ttc att gaa gct ttg agg 1529
140 Glu Arg Trp Thr Glu Glu Glu His Asn Arg Phe Ile Glu Ala Leu Arg
141 25 30 35 40

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145          45          50
147 atatgtctta ttttttgtgt ttgcagaggt ttgtcttcaa actgatttgc tttttttcat 1640
149 ttggacag aa cat gta gca aca aaa act gct gtc cag ata aga agt cac 1689
150          Glu His Val Ala Thr Lys Thr Ala Val Gln Ile Arg Ser His
151          55          60
153 gct cag aaa ttt ttc tcc aag gtaaaatcgg ttaattttga aatgatgttc 1740
154 Ala Gln Lys Phe Phe Ser Lys
155 65          70
157 tcatcttcat tggcttaatg cttaagactt attgaaagcc aggcaagttt tctgcttctt 1800
159 ttgcttctta gtcaggagat agatagatta cgttttttaga gtttagtaat gagcaataag 1860
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163 ttgttaatcc acaaacatgt acatagattc ttcagaagaa tgtagtttc tttagattct 1980
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169 ttctgtcatt taaacttgtt aggtgtcatt agatttttgt ttgtttacgt ttgtttagag 2160
171 ggtaacaaaa ctactctcat ctctctcag gta gag aaa gag gct gaa gct aaa 2213
172          Val Glu Lys Glu Ala Glu Ala Lys
173          75
175 ggt gta gct atg ggt caa gcg cta gac ata gct att cct cct cca cgg 2261
176 Gly Val Ala Met Gly Gln Ala Leu Asp Ile Ala Ile Pro Pro Pro Arg
177 80          85          90          95
179 cct aag cgt aaa cca aac aat cct tat cct cga aag acg gga agt gga 2309
180 Pro Lys Arg Lys Pro Asn Asn Pro Tyr Pro Arg Lys Thr Gly Ser Gly
181          100          105          110
183 acg atc ctt atg tca aaa acg ggt gtg aat gat gga aaa gag tcc ctt 2357
184 Thr Ile Leu Met Ser Lys Thr Gly Val Asn Asp Gly Lys Glu Ser Leu
185          115          120          125
187 gga tca gaa aaa gtg tcg cat cct gag gtgattttca tggatcatatg 2404
188 Gly Ser Glu Lys Val Ser His Pro Glu
189          130          135
191 gcacgttttt gcagtgtgtc acattgctcc tcatgttatt aatacagatt gtgtgcttcg 2464
193 tttatag atg gcc aat gaa gat cga caa caa tca aag cct gaa gag aaa 2513
194          Met Ala Asn Glu Asp Arg Gln Gln Ser Lys Pro Glu Glu Lys
195          140          145          150
197 act ctg cag gaa gac aac tgt tca gat tgt ttc act cat cag tat ctc 2561
198 Thr Leu Gln Glu Asp Asn Cys Ser Asp Cys Phe Thr His Gln Tyr Leu
199          155          160          165
201 tct gct gca tcc tcc atg aat aaa agt tgt ata gag aca tca aac gca 2609
202 Ser Ala Ala Ser Ser Met Asn Lys Ser Cys Ile Glu Thr Ser Asn Ala
203          170          175          180
205 agc act ttc cgc gag ttc ttg cct tca cgg gaa gag gtaaaaaaca 2655
206 Ser Thr Phe Arg Glu Phe Leu Pro Ser Arg Glu Glu
207          185          190
209 atcttttcatt gctattttgag gttttaagac gattagtaact tttcatgaaa ctaaaaccgt 2715
211 gggggaataa cag gga agt cag aat aac agg gta aga aag gag tca aac 2764
212          Gly Ser Gln Asn Asn Arg Val Arg Lys Glu Ser Asn
213          195          200          205

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217				210					215					220			
219	cag	act	tat	ccg	atg	cat	atc	cct	gtg	cta	gtg	cca	ttg	ggg	agc	tca	2860
220	Gln	Thr	Tyr	Pro	Met	His	Ile	Pro	Val	Leu	Val	Pro	Leu	Gly	Ser	Ser	
221			225					230					235				
223	ata	aca	agt	tct	cta	tca	cat	cct	cct	tca	gag	cca	gat	agt	cat	ccc	2908
224	Ile	Thr	Ser	Ser	Leu	Ser	His	Pro	Pro	Ser	Glu	Pro	Asp	Ser	His	Pro	
225		240					245						250				
227	cac	aca	gtt	gca	gga	gat	tat	cag	tcg	ttt	cct	aat	cat	ata	atg	tca	2956
228	His	Thr	Val	Ala	Gly	Asp	Tyr	Gln	Ser	Phe	Pro	Asn	His	Ile	Met	Ser	
229	255					260					265				270		
231	acc	ctt	tta	caa	aca	ccg	gct	ctt	tat	act	gcc	gca	act	ttc	gcc	tca	3004
232	Thr	Leu	Leu	Gln	Thr	Pro	Ala	Leu	Tyr	Thr	Ala	Ala	Thr	Phe	Ala	Ser	
233					275						280				285		
235	tca	ttt	tgg	cct	ccc	gat	tct	agt	ggt	ggc	tca	cct	gtt	cca	ggg	aac	3052
236	Ser	Phe	Trp	Pro	Pro	Asp	Ser	Ser	Gly	Gly	Ser	Pro	Val	Pro	Gly	Asn	
237				290					295				300				
239	tca	cct	ccg	aat	ctg	gct	gcc	atg	gcc	gca	gcc	act	gtt	gca	gct	gct	3100
240	Ser	Pro	Pro	Asn	Leu	Ala	Ala	Met	Ala	Ala	Ala	Thr	Val	Ala	Ala	Ala	
241			305					310					315				
243	agt	gct	tgg	tgg	gct	gcc	aat	gga	tta	tta	cct	tta	tgt	gct	cct	ctt	3148
244	Ser	Ala	Trp	Trp	Ala	Ala	Asn	Gly	Leu	Leu	Pro	Leu	Cys	Ala	Pro	Leu	
245		320					325					330					
247	agt	tca	ggt	ggt	ttc	act	agt	cat	cct	cca	tct	act	ttt	gga	cca	tca	3196
248	Ser	Ser	Gly	Gly	Phe	Thr	Ser	His	Pro	Pro	Ser	Thr	Phe	Gly	Pro	Ser	
249	335				340						345				350		
251	tgt	gat	gta	gag	tac	aca	aaa	gca	agc	act	tta	caa	cat	ggt	tct	gtg	3244
252	Cys	Asp	Val	Glu	Tyr	Thr	Lys	Ala	Ser	Thr	Leu	Gln	His	Gly	Ser	Val	
253					355					360					365		
255	cag	agc	cga	gag	caa	gaa	cac	tcc	gag	gca	tca	aag	gct	cga	tct	tca	3292
256	Gln	Ser	Arg	Glu	Gln	Glu	His	Ser	Glu	Ala	Ser	Lys	Ala	Arg	Ser	Ser	
257					370					375				380			
259	ctg	gac	tca	gag	gat	gtt	gaa	aat	aag	agt	aaa	cca	gtt	tgt	cat	gag	3340
260	Leu	Asp	Ser	Glu	Asp	Val	Glu	Asn	Lys	Ser	Lys	Pro	Val	Cys	His	Glu	
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263	cag	cct	tct	gca	aca	cct	gag	agt	gat	gca	aag	ggt	tca	gat	gga	gca	3388
264	Gln	Pro	Ser	Ala	Thr	Pro	Glu	Ser	Asp	Ala	Lys	Gly	Ser	Asp	Gly	Ala	
265		400					405					410					
267	gga	gac	aga	aaa	caa	gtt	gac	cgg	tcc	tcg	tgt	ggc	tca	aac	act	ccg	3436
268	Gly	Asp	Arg	Lys	Gln	Val	Asp	Arg	Ser	Ser	Cys	Gly	Ser	Asn	Thr	Pro	
269	415					420						425				430	
271	tcg	agt	agt	gat	gat	gtt	gag	gcg	gat	gca	tca	gaa	agg	caa	gag	gat	3484
272	Ser	Ser	Ser	Asp	Asp	Val	Glu	Ala	Asp	Ala	Ser	Glu	Arg	Gln	Glu	Asp	
273					435					440					445		
275	ggc	acc	aat	ggt	gag	gtg	aaa	gaa	acg	aat	gaa	gac	act	aat	aaa	cct	3532
276	Gly	Thr	Asn	Gly	Glu	Val	Lys	Glu	Thr	Asn	Glu	Asp	Thr	Asn	Lys	Pro	
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279	caa	act	tca	gag	tcc	aat	gca	cgc	cgc	agt	aga	atc	agc	tcc	aat	ata	3580

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288                               Gly Arg
289                               490
291 att gcc ttc caa gct ctc ttc tcc aga gag gta ttg ccg caa agt ttt 3734
292 Ile Ala Phe Gln Ala Leu Phe Ser Arg Glu Val Leu Pro Gln Ser Phe
293          495          500          505
295 aca tat cga gaa gaa cac aga gag gaa gaa caa caa caa caa gaa caa 3782
296 Thr Tyr Arg Glu Glu His Arg Glu Glu Glu Gln Gln Gln Gln Glu Gln
297          510          515          520
299 aga tat cca atg gca ctt gat ctt aac ttc aca gct cag tta aca cca 3830
300 Arg Tyr Pro Met Ala Leu Asp Leu Asn Phe Thr Ala Gln Leu Thr Pro
301          525          530          535
303 gtt gat gat caa gag gag aag aga aac aca gga ttt ctt gga atc gga 3878
304 Val Asp Asp Gln Glu Glu Lys Arg Asn Thr Gly Phe Leu Gly Ile Gly
305          540          545          550
307 tta gat gct tca aag cta atg agt aga gga aga aca ggt ttt aaa cca 3926
308 Leu Asp Ala Ser Lys Leu Met Ser Arg Gly Arg Thr Gly Phe Lys Pro
309 555          560          565          570
311 tac aaa aga tgt tcc atg gaa gcc aaa gaa agt aga atc ctc aac aac 3974
312 Tyr Lys Arg Cys Ser Met Glu Ala Lys Glu Ser Arg Ile Leu Asn Asn
313          575          580          585
315 aat cct atc att cat gtg gaa cag aaa gat ccc aaa cgg atg cgg ttg 4022
316 Asn Pro Ile Ile His Val Glu Gln Lys Asp Pro Lys Arg Met Arg Leu
317          590          595          600
319 gaa act caa gct tcc aca tga gactctatct tcactctgac tggtgtttgt 4073
320 Glu Thr Gln Ala Ser Thr
321          605
323 actctgtttt taagttttca agaccactgc tacattttct ttttcttttg aggcctttgt 4133
325 atttgtttcc ttgtccatag tcttctgtga acatttgact ctgtattatt caacaaatca 4193
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347 Asn Arg Phe Ile Glu Ala Leu Arg Leu Tyr Gly Arg Ala Trp Gln Lys

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VERIFICATION SUMMARY

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Input Set : A:\PTO.DC.txt

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L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date